

Kosuke Hashimoto

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,689
citations

361413

20
h-index

395702

33
g-index

42
all docs

42
docs citations

42
times ranked

5217
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
2	KEGG as a glycome informatics resource. <i>Glycobiology</i> , 2006, 16, 63R-70R.	2.5	279
3	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566.	21.4	271
4	Phosphorylation in Protein-Protein Binding: Effect on Stability and Function. <i>Structure</i> , 2011, 19, 1807-1815.	3.3	246
5	Single-cell transcriptomics reveals expansion of cytotoxic CD4 T cells in supercentenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24242-24251.	7.1	215
6	Mechanisms of protein oligomerization, the critical role of insertions and deletions in maintaining different oligomeric states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20352-20357.	7.1	160
7	The repertoire of desaturases and elongases reveals fatty acid variations in 56 eukaryotic genomes. <i>Journal of Lipid Research</i> , 2008, 49, 183-191.	4.2	150
8	Cancer Missense Mutations Alter Binding Properties of Proteins and Their Interaction Networks. <i>PLoS ONE</i> , 2013, 8, e66273.	2.5	102
9	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018.	12.8	98
10	Caught in self-interaction: evolutionary and functional mechanisms of protein homooligomerization. <i>Physical Biology</i> , 2011, 8, 035007.	1.8	94
11	Prediction of glycan structures from gene expression data based on glycosyltransferase reactions. <i>Bioinformatics</i> , 2005, 21, 3976-3982.	4.1	78
12	Prevention of hepatocellular carcinoma by targeting MYCN-positive liver cancer stem cells with acyclic retinoid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4969-4974.	7.1	78
13	CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. <i>Genome Research</i> , 2015, 25, 1812-1824.	5.5	49
14	Large-scale mapping of human protein interactome using structural complexes. <i>EMBO Reports</i> , 2012, 13, 266-271.	4.5	43
15	Functional States of Homooligomers: Insights from the Evolution of Glycosyltransferases. <i>Journal of Molecular Biology</i> , 2010, 399, 196-206.	4.2	39
16	Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. <i>Carbohydrate Research</i> , 2009, 344, 881-887.	2.3	37
17	Evolutionary, Physicochemical, and Functional Mechanisms of Protein Homooligomerization. <i>Progress in Molecular Biology and Translational Science</i> , 2013, 117, 3-24.	1.7	34
18	Mining significant tree patterns in carbohydrate sugar chains. <i>Bioinformatics</i> , 2008, 24, i167-i173.	4.1	33

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19	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. <i>Journal of Virology</i> , 2016, 90, 10811-10822.	3.4	27
20	Oncogenic potential is related to activating effect of cancer single and double somatic mutations in receptor tyrosine kinases. <i>Human Mutation</i> , 2012, 33, 1566-1575.	2.5	26
21	DUX4 is a multifunctional factor priming human embryonic genome activation. <i>IScience</i> , 2022, 25, 104137.	4.1	20
22	AN IMPROVED SCORING SCHEME FOR PREDICTING GLYCAN STRUCTURES FROM GENE EXPRESSION DATA. , 2007, , .		18
23	Deficiency of multidrug resistance 2 contributes to cell transformation through oxidative stress. <i>Carcinogenesis</i> , 2016, 37, 39-48.	2.8	15
24	Nuclear transcriptome profiling of induced pluripotent stem cells and embryonic stem cells identify non-coding loci resistant to reprogramming. <i>Cell Cycle</i> , 2015, 14, 1148-1155.	2.6	14
25	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
26	A new efficient probabilistic model for mining labeled ordered trees applied to glycobiology. <i>ACM Transactions on Knowledge Discovery From Data</i> , 2008, 2, 1-30.	3.5	10
27	Mutations that reduce its specific DNA binding inhibit high NaCl-induced nuclear localization of the osmoprotective transcription factor NFAT5. <i>American Journal of Physiology - Cell Physiology</i> , 2012, 303, C1061-C1069.	4.6	10
28	The repertoire of desaturases for unsaturated fatty acid synthesis in 397 genomes. <i>Genome Informatics</i> , 2006, 17, 173-83.	0.4	9
29	STAP cells are derived from ES cells. <i>Nature</i> , 2015, 525, E4-E5.	27.8	8
30	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. <i>Genome Research</i> , 2021, 31, 1983-1993.	5.5	7
31	A global representation of the carbohydrate structures: a tool for the analysis of glycan. <i>Genome Informatics</i> , 2005, 16, 214-22.	0.4	7
32	Characterization of Novel Transcripts of Human Papillomavirus Type 16 Using Cap Analysis Gene Expression Technology. <i>Journal of Virology</i> , 2015, 89, 2448-2452.	3.4	6
33	Extraction of species-specific glycan substructures. <i>Genome Informatics</i> , 2004, 15, 69-81.	0.4	5
34	KEGG GLYCAN for Integrated Analysis of Pathways, Genes, and Structures. , 2008, , 441-444.		3
35	Use of Cap Analysis Gene Expression to detect human papillomavirus promoter activity patterns at different disease stages. <i>Scientific Reports</i> , 2020, 10, 17991.	3.3	1
36	KEGG GLYCAN for Integrated Analysis of Pathways, Genes, and Glycan Structures. , 2010, , 197-210.		0